

SEQ ID NO: 6 A33 1 M V G K M W P V L W T L C A V R V T V D A I S V E T P Q D V L R A S Q G K S V T L P C T Y H T S T S
SEQ ID NO: 1 40628 1 M G T K A Q V E R K L L C L F I L A I L L C S L A L G S V T V H S S E P E V R I P E
SEQ ID NO: 2 45416 1 M G I L L G L L L G H L T V D T Y G R P I L E V P E S V T G P W K G D V N L P C T Y D P L
SEQ ID NO: 9 35638 1 M A R R S R H R L L L L L R Y L V V A L G Y H K A Y G F S A P K D Q Q V T A V E
SEQ ID NO: 10 JAM 1 . M G T E G K A G R K L L F L F T S M I L G S L V Q G K G S V Y T A Q S D V Q V P E

A33 51 S R E G L I Q W D K L L L T H T E R V V I W P F S N K N Y I H G E L Y K N R V S I S N H A E Q S D A
40628 43 N N P V K L S C A Y S G F S S P R V E W K F D Q G D T T R L V C Y N N K I T A S Y E D R V T F L P T
45416 47 Q G Y T Q V L Y K W L V Q R G S D P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H K V P G D V
35638 43 Y Q E A I L A C K T P K X T V S S R L E W K L G R S V S F Y Y Q Q T L Q G D F K N R A E M I D F
JAM 42 H E S I K L T C T Y S G F S S P R V E W K F V Q G S T T A L V C Y N S Q I T A P Y A D R V T F S S S

A33 101 S I T I D Q L T M A D N G T Y E C S V S L . M S D L E G N T K S R V R L L V L V P P S K
40628 93 G I T F K S V T R E D T G T Y T C M V S E E G G N S Y G E V K V K L I V L V P P S K
45416 97 S L Q L S T L E M D D R S H Y T C E V T W Q T P D G N Q V V R D K I T E L R V Q K L S V S K P T V T
35638 93 H I R I K N V T R S D A G K Y R C E V S A P S E Q G Q N L E E D T V T L E V L V A P A V
JAM 92 G I T F S S V T R K D N G E Y T C M V S E E G G Q N Y G E V S I H L T V L V P P S K

A33 144 P E C G I E G E T I I G N N I Q L T C Q S K E G S P T P O Y S W K R Y N I L N Q E Q
40628 135 P T V N I P S S A T I G N R A V L T C S E Q D G S P P S E Y T W F K D G I V M P T N . P K S T R A F
45416 147 T G S G Y G F T V P Q G M R I S L Q C Q A R . G S P P I S Y I W Y K Q O T N N Q E P
35638 137 P S C E V P S S A L S G T V V E L R C Q D K E G N P A P E Y T W F K D G I R L L E N . P R L G S Q S
JAM 134 P T I S V P S S V T I G N R A V L T C S E H D G S P P S E Y S W F K D G I S M L T A D A K K T R A F

FIG.-1A

SEQ ID NO: 6 A33 186 ... PLAQPASGQPVSLKNISSTDTSGYIICITSSNEEG... TQFCNITY
SEQ ID NO: 1 40628 184 SNSSYVLNPTTGEELVFDPLSASDTGEYSCEARNGYG... TPMTSNAY
SEQ ID NO: 2 45416 188 ... IKVATLSTLLFKPAVIA DSGSYFCTAKGQVGSSEQHSDIVKFFVVKD
SEQ ID NO: 9 35638 186 TNSSYTMNTKTGTLLQFNTVS KLD TGEYSCEARN SVG... YRRCPGKR
SEQ ID NO: 10 JAM 184 MNSSTIDPKSGDLIFDPVTA FDSGEY YCAQN GYG... TAMRSEAA

A33 227 AVRSPSMNVALYVGIAGVGVAA LIIIGII YCCCCRGKDDNTTEOKEDA...
40628 228 MEAEVERNVGIVAAVLVTLILLGILVFGIWFAYSRGHFDRTKKGT S...
45416 233 SKLLKTKTEAPTTMTYPLKATSTYKQSWDWT TDM DGYLGETSAGPGKSL
35638 230 MQVDDLHISGIIAAVVVVALVISVCGLGVCYARQKGYFSKETSFQKS...
JAM 228 HMDA VELNVGGIVAAVLVTLILLGLLIFGVWFAYSRGYFETTKKGTAP...

A33 275 RPNREAYEEPPEQLREL SRERE EDDYRQEEQRSTGRES PDHLDQ
40628 275 ... SKKV IYSQPSARS EGEFKQTS SFLV...
45416 283 PVFAIILISLCCMVVFTMAYIMLCRKTSQOEHVVEAAR...
35638 277 NSSSKATTMSENVQWLTPIPALWKAAAGGSRGQEF...
JAM 276 ... GKKV IYSQPSSTRSEGEFKQTS SFLV...

FIG. 1B

SEQ ID NO:1

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr
 1 5 10 15 20 25 30
 Val His Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val
 35 40 45 50 55 60
 Glu Trp Lys Phe Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu
 65 70 75 80 85 90
 Pro Thr Gly Ile Thr Phe Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser Glu Glu Gly Asn Ser Tyr Gly
 95 100 105 110 115 120
 Glu Val Lys Val Lys Leu Ile Val Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr Ile Gly Asn Arg Ala Val
 125 130 135 140 145 150
 Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn Pro Lys Ser Thr
 155 160 165 170 175 180
 Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly Glu Tyr
 185 190 195 200 205 210
 Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
 215 220 225 230 235 240
 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys
 245 250 255 260 265 270
 Lys Gly Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
 275 280 285 290 295 299

FIG.-2

SEQ ID NO:2
 1 MGILLGILL GHLTVDTYGR PILEVPESVT GPWKGDVNL P CTYDPLQGYT QVLVKWLVR GSDPVTIFLR DSSGDHIQQA KYQRLHVSH KVPGDVSLQL
 101 STLEMDRSH YTCEVTWQTP DGNQVVRDKI TELRVQKLSV SKPTVTTCG YGFTVPQGMRLSLQCCARGSPPISYIWKQ QTNQEPKIV ATLSTLLFKP
 ^Glycosaminoglycan attachment site
 201 AVIADSGSYF CTAKGVQSE QHSDIVKFVV KDSSKLLKTK TEAPTTMTYP LKATSTVKQS WDWTDMDGY LGETSAGPGK SLPVFAIILI ISLCCMVVFT
 ^Transmembrane domain

FIG._3

301 MAYIMLCRKT SQEHVVEAA R

OLI2162 (35936.f1)
 SEQ ID NO:12
 TCGCGGAGCTGTGTTCTGTTTCCC
 OLI2163 (35936.p1)
 SEQ ID NO:13
 TGATCGGATGGGACAAAGCGCAAGCTCGAGAGGAACTGTTGTGCCT
 OLI2164 (35936.f2)
 SEQ ID NO:14
 ACACCTGGTTCAAAGATGGG
 OLI2165 (35936.r1)
 SEQ ID NO:15
 TAGGAAGAGTTGCTGAAGGCACGG

4 / 24

OLI2166 (35936.f3)
 SEQ ID NO:16
 TTGCCTTACTCAGGTGCTAC
 OLI2167 (35936.r2)
 SEQ ID NO:17
 ACTCAGCAGTGGTAGGAAAG

FIG._8

DNA35936 SEQ ID NO:3

CTTCTTGCCA ACTGGTATCA CCTTCAAGTC CGTGACACGG GAAGACACTG 50
GGACATACAC TTGTATGGTC TCTGAGGAAG GCGGCAACAG CTATGGGGAG 100
GTCAAGGTCA AGCTCATCGT GCTTGTGCCT CCATCCAAGC CTACAGTTAA 150
CATCCCCTCC TCTGCCACCA TTGGGAACCG GGCAGTGCTG ACATGCTCAG 200
AACAAGATGG TTCCCCACCT TCTGAATACA CCTGGTTCAA AGATGGGATA 250
GTGATGCCTA CGAATCCCAA AAGCACCCGT GCCTTCAGCA ACTCTTCCTA 300
TGTCTGAAT CCCACAACAG GAGAGCTGGT CTTTGATCCC CTGTCAGCCT 350
CTGATACTGG AGAATACAGC TGTGAGGCAC GGAATGGGTA 390

FIG._4A

consen01 SEQ ID NO:4

TCTCAGTCCC CTCGCTGTAG TCGCGGAGCT GTGTTCTGTT TCCCAGGAGT 50
CCTTCGGCGG CTGTTGTGCT CAGGTGCGCC TGATCGCGAT GGGGACAAAG 100
GCGCAAGCTC GAGAGGAAAC TGTGTGCCT CTTCATATTG GCGATCCTGT 150
TGTGCTCCCT GGCATTGGGC AGTGTTACAG TTGCACTCTT CTGAACCTGA 200
AGTCAGAATT CCTGAGAATA ATCCTGTGAA GTTGTCTGTG GCCTACTCGG 250
GCTTTTCTTC TCCCCGTGTG GAGTGGAAGT TTGACCAAGG AGACACCACC 300
AGACTCGTTT GCTATAATAA CAAGATCACA GCTTCCTATG AGGACCGGGT 350
GACCTTCTTG CCAACTGGTA TCACCTTCAA GTCCGTGACA CGGGAAGACA 400
CTGGGACATA CACTTGTATG GTCTCTGAGG AAGGCGGCAA CAGCTATGGG 450
GAGGTCAAGG TCAAGCTCAT CGTGCTTGTG CCTCCATCCA AGCCTACAGT 500
TAACATCCCC TCCTCTGCCA CCATTGGGAA CCGGGCAGTG CTGACATGCT 550
CAGAACAAGA TGGTTCCCCA CCTTCTGAAT ACACCTGGTT CAAAGATGGG 600
ATAGTGATGC CTACGAATCC CAAAAGCACC CGTGCCTTCA GCAACTCTTC 650
CTATGTCCTG AATCCCACAA CAGGAGAGCT GGTCTTTGAT CCCCTGTCAG 700
CCTCTGATAC TGGAGAATAC AGCTGT 726

FIG._4B

consen02 SEQ ID NO:5

GCAGGCAAAG TACCAGGGCC GCCTGCATGT GAGCCACAAG GTTCCAGGAG 50
ATGTATCCCT CCAATTGAGC ACCCTGGAGA TGGATGACCG GAGCCACTAC 100
ACGTGTGAAG TCACCTGGCA GACTCCTGAT GGCAACCAAG TCGTGAGAGA 150
TAAGATTACT GAGCTCCGTG TCCAGAACT CTCTGTCTCC AAGCCCACAG 200
TGACAACTGG CAGCGGTTAT GGCTTCACGG TGCCCCAGGG AATGAGGATT 250
AGCCTTCAAT GCCAGGGTTC GGGGTTCTCC TCCCATCAGT TATATTTGGT 300
ATAAGCAACA GACTAATAAC CAGGGAACCC ATCAAAGTAG CAACCCTAAG 350
TACCTTACTC TTCAAGCCTG CGGTGATAGC CGACTCAGGC TCCTATTTCT 400
GCACTGCCAA GGGCCAGGTT GGCTCTGAGC AGCACAGCGA CATTGTGAAG 450
TTTGTGGTCA AAGACTCCTC AAAGCTACTC AAGACCAAGA CTGAGGCACC 500
TACAACCATG ACATACCCCT TGAAAGCAAC ATCTACAGTG AAGCAGTCCT 550
GGGACTGGAC CACTGACATG GATGGCTACC TTGGAGAGAC CAGTGCTGGG 600
CCAGGAAAGA GCCTGCCTGT CTTTGCCATC ATCCTCATCA TCTCCTTGTTG 650
CTGTATGGTG GTTTTTACCA TGGCCTATAT CATGCTCTGT CGGAAGACAT 700
CCCAACAAGA GCATGTCTAC GAAGCAGCCA GGGCACATGC CAGAGAGGCC 750
AACGACTCTG GAGAAACCAT GAGGGTGGCC ATCTTCGCAA GTGGCTGCTC 800
CAGTGATGAG CCAACTTCCC AGAATCTGGG GCAACAATA CTCTGATGAG 850
CCCTGCATAG GACAGGAGTA CCAGATCATC GCCCAGATCA ATGGCAACTA 900
CGCCCGCCTG CTGGACACAG TTCCTCTGGA TTATGAGTTT CTGGCCACTG 950
AGGGCAAAAG TGTCTGTAA AAATGCCCCA TTAGGCCAGG ATCTGCTGAC 1000
ATAATTGCCT AGTCAGTCCT TGCCTTCTGC ATGGCCTTCT TCCCTGCTAC 1050
CTCTCTTCCT GGATAGCCCA AAGTGTCGCG CTACCAACAC TGGAGCCGCT 1100
GGGAGTCACT GGCTTTGCCC TGAATTTGTC CAGATGCATC TCAAGTAAGC 1150
CAGCTGCTGG ATTTGGCTCT GGGCCCTTCT AGTATCTCTG CCGGGGGCTT 1200
CTGGTACTCC TCTCTAAATA CCAGAGGGAA GATGCCATA GCACTAGGAC 1250
TTGGTCATCA TGCCTACAGA CACTATTCAA CTTTGGCATC TTGCCACCAG 1300
AAGACCCGAG GGGAGGCTCA GCTCTGCCAG CTCAGAGGAC CAGCTATATC 1350
CAGGATCATT TCTCTTTCTT CAGGGCCAGA CAGCTTTTAA TTGAAATTGT 1400
TATTTACAG GCCAGGGTTC AGTTCTGCTC CTCCACTATA AGTCTAATGT 1450
TCTGACTCTC TCCTGGTGCT CAATAAATAT CTAATCATAA CAGCAAAAAA 1500
AAA 1503

FIG. 4C

SEQ ID NO:11 GGAGTCCTT CGGCGGCTGT TGTGTCAATG GCCTGATCGC GATGGGGACA AAGGGGCAAG TCGAGAGGAA ACTGTTGTGC CTCTTCATAT 100
TGGCGATCCT GTTGTGCTCC CTGGCAATTGG GCAGTGTATC AGTGCACTCT TCTGAACCTG AAGTCAGAAT TCCTGAGAAT AATCCTGTGA AGTTGTCTCTG 200
TGCCTACTCG GGCTTTTCTT CTCCCGGTGT GGAGTGGGAG TTGACCAAG GAGACACCAC CAGACTCGTT TGCTATAATA ACAAGATCAC AGCTTCTCTAT 300
GAGGACCGGG TGACCTTCTT GCCAACTGGT ATCACCCTCA AGTCCGTGAC ACGGGAAGAC ACTGGGACAT ACACCTGTAT GGTCTCTGAG GAAGCGGCA 400
ACAGCTATGG GGAGGTCAAG GTCAAGCTCA TCGTGTCTGT GCCTCCATCC AAGCCTACAG TTAACATCCC CTCTCTGCC ACCATTGGGA ACCGGGCAGT 500
GCTGACATGC TCAGAACAAAG ATGGTTCCCC ACCTTCTGAA TACACCTGGT TCAAAGATGG GATAGTGATG CCTACGAATC CCAAAAGCAC CCGTGCCCTTC 600
AGCAACTCTT CCTATGTCCT GAATCCACCA ACAGGAGAGC TGGTCTTTGA TCCCCTGTCA GCCTCTGATA CTGGAGAATA CAGCTGTGAG GCACGGAATG 700
GGTATGGGAC ACCCATGACT TCAAATGCTG TGGCATGGA AGCTGTGGAG CGGAATGTGG GGGTCATCGT GGCAGCCGTC CTTGTAACCC TGATTCTCCT 800
GGGAATCTTG GTTTTGGCA TCTGGTTTGC CTATAGCCGA GGCCACTTTG ACAGAACAAG GAAAGGGACT TCGAGTAAGA AGGTGATTGA CAGCCAGCCT 900
AGTGCCCGAA GTGAAGGAGA ATTCAAAACAG ACCTCGTCAAT TCCTGGTGTG AGCCTGGTGC CTCTACACC GCTCACCACC TATCATCTGC ATTTGCCTTA CTCAGGTGCT 1000
ACCGGACTCT GGCCCTGAT GTCTGTAGTT TCACAGGATG CCTTATTGT CTCTACACC CCACAGGGCC CCTACTTCT TCGGATGTGT TTTTAATAAT 1100
GTCAGCTATG TGGCCCATCC TCCTTCATGC CCTCCCTCCC TTTCCTACCA CTGCTGAGTG GCCTGGAACT TGTTTAAAGT GTTTATTCCC CATTTCTTTG 1200
AGGGATCAGG AAGGAATCCT GGGTATGCCA TTGACTTCCC TTCTAAGTAG ACAGCAAAA TGGCGGGGGT CGCAGGAATC TGCACCTAAC TGCCACCTG 1300
GCTGGCAGGG ATCTTTGAAT AGGTATCTTG AGCTTGGTTC TGGGCTCTTT CCTTGTGTAC TGACGACCAG GGCCAGCTGT TCTAGAGCGG GAATTAGAGG 1400
CTAGAGCGGC TGAATGGTT GTTTGGTGAT GACACTGGGG TCCTTCCATC TCTGGGGCCC ACTCTCTTCT GTCTTCCCAT GGGAAAGTGC ACTGGGATCC 1500
CTCTGCCCTG TCCTCCTGAA TACAAGCTGA CTGACATTGA CTGTGTCTGT GGAAAATGG AGCTCTTGT GTGGAGAGCA TAGTAAATTT TCAGAGAACT 1600
TGAAGCCAAA AGGATTTAA ACCGCTGCTC TAAAGAAAAG AAAACTGGAG GCTGGGCGCA GTGGCTCAG CCTGTAAATC CAGAGGCTGA GGCAGGCGGA 1700
TCACCTGAGG TCGGGAGTTC GGGATCAGCC TGACCAACAT GGAGAAACCC TACTGGAAAT ACAAGTTAG CCAGGCATGG TGGTGCATGC CTGTAGTCCC 1800
AGCTGCTCAG GAGCCTGGCA ACAAGAGCAA AACTCCAGCT CA 1842

FIG._5

SEQ ID NO:7

```

1 CCCACGGCTC CGCCACGGCG TCCGCCGCCA CGGCTCCGGG CCACCAGNAG TTGAGCCTC TTGAGTACCA GGAGGCTGGA AGAAGGACA
GGGTGGCAG CGGGGTGGCG AGGCGGTGCC CCAGCGGGGT GCGAGGGCC GGTGCTCTTC AACTCGGAG AAACCATCGT CCTCCGACCT TCTTCTCTGT

101 GAAGTAGCTC TGGCTGTGAT GGGGATCTTA CTGGCCTGCC TACTCTCTGG GCACCTAACA GTGCACACTT ATGCCCGTCC CATCTCGAA GTGCCAGAGA
CTTCATCGAG ACCGACACTA CCCCTAGAAT GACCCGGACG ATCAGGACCC CGTGGATTGT CACCTGTGAA TACCGGCAGG GTAGGACCTT CACGGTCTCT
1      SEQ ID NO:2 M G I L L G L L L G H L T V D T Y G R P I L E V P E S
^MET

201 GTGTAACAGG ACCTTGAAA GGGGATGTGA ATCTTCCCTG CACCTATGAC CCCCTGCAAG CCTACACCCA AGTCTTGGTG AAGTGGCTGG TACAACGTGG
CACATTGTCC TGGAACTTTT CCCCTACACT TAGAAGGGAC GTGGATACTG GGGGACGTTT CGATGTGGT TCAGAACCAC TTCACCGACC ATGTTGCACC
29 V T G P W K G D V N L P C T Y D P L Q G Y T Q V L V K W L V Q R G

301 CTCAGACCTT GTCACCATCT TTCTAGGTGA CTCTTCTGGA GACCATATCC ACCAGGCCAA GTACCAGGGC CCCCTGCATG TCAGCCACAA GGTTCAGGA
GAGTCTGGGA CAGTGGGTAGA AAGATGCACT GAGACACCT CTGCTATAGG TCCTCGGTTT CATGTCCCG GCGGACGTAC ACTCGGTGTT CCAAGGTCTT
62 S D P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H K V P G

401 GATGTATCCC TCCAATTGAG CACCTTGGAG ATGGATGACC GGAGCCACTA CACCTGTGAA CTCACCTGGC AGACTCCTGA TGGCAACCAA GTCGTGAGAG
CTACATAGG AGGTTAACTC GTGGGACCTC TACCTACTGG CCTCGGTGAT GTGCACACTT CACTGGACCG TCTGAGGACT ACCGTTGTT CAGCACTCTC
95 D V S L Q L S T L E M D D R S H Y T C E V T W Q T P D G N Q V V R D

501 ATAAGATTAC TCAGTCTCGT GTCCAGAAAC TCTCTGTCTC CAAGCCACA GTACACACTG GCAGCGGTTA TGCCTTCACG TGCCCCCAGG GAATGAGGAT
TATTCTAATG ACTCGAGGCA CAGGTCTTTG AGAGACAGAG GTTCGGGTGT CACTGTTGAC CGTCGCCAAT ACCGAAGTCC CACGGGTGCC CTTACTCCTA
129 K I T E L R V Q K L S V S K P T V T T G S G Y G F T V P Q G H R I

601 TAGCCTTCAA TGCCAGGCTC GGGGTTCTCC TCCCATCAGT TATATTGTTG ATAGCAACA GACTAATAAC CAGGAACCCA TCAAAGTAGC AACCCTAAGT
ATCGGAAGTT ACGGTCCGAG CCCCAGAGG AGGGTAGTCA ATATAAACCA TATTCGTTGT CTCATTATTG GTCCTTGGGT AGTTTCATCG TTGGGATTCA
162 S L Q C Q A R G S P P I S Y I W Y K Q Q T N N Q E P I K V A T L S

```

FIG. 6A

SEQ ID NO:7 701 ACCTTACTCT TCAAGCCTGC GGTGATAGCC GACTCAGCCT CCTATTTCGT CACTGCCAAG GGCCAGGTTG GCTCTGAGCA GCACAGCGAC ATTGTGAAGT
TGGNATGAGA AGTTCGGACG CCACTATCGG CTCAGTCCGA GGATAAGAC GTGACGGTTC CCGGTCCAAC CGAGACTCGT CGTGTGCTG TAACACTTCA

SEQ ID NO:2 195 T L L F K P A V I A D S G S Y F C T A K G Q V G S E Q H S D I V K F

801 TTGTGGTCAA AGACTCCTCA AAGCTACTCA AGACCAAGAC TGAGGCACCT ACAACCATGA CATACCCTT GAAAGCAACA TCTACAGTGA AGCAGTCCTG
AACACCAGTT TCTGAGGAGT TTCGATGAGT TCTGGTCTG ACTCCGTGGA TCTTGTACT GTATGGGAA CTTTCGTTGT AGATGTCAC TCGTCAGGAC

229 V V K D S S K L L K T K T E A P T T M T Y P L K A T S T V K Q S W

901 GGA CTGGACC ACTGACATGG ATGGCTACCT TGGAGAGACC AGTCTGGCC CAGGAAGACG CCTGCTGTC TTTCCCATCA TCCTCATCAT CTCCTTGTGC
CCTGACCTGG TCACTGTACC TACCGATGGA ACCTCTCTGG TCACGACCGG GTCTTTCTC GGACGGACAG AAACGGTAGT AGCAGTAGTA GAGGAACACG

262 D W T T D M D G Y L G E T S A G P G K S L P V F A I I L I I S L C

1001 TGTATGGTGG TTTTACCAT GGCCTATATC ATGCTCTGTC GGAAGACATC CCAACACAG CATCTCTACG AACGAGCCAG CTAAGAAAGT CTCCTCTCTT
ACATACCACC AAAAATGGTA CCGGATATAG TACGAGACAG CCTTCTGTAG GGTCTGTCTC GTACAGATGC TTCTGCGTC CATTCCTTCA GAGAGGAGAA

295 C H V V F T M A Y I M L C R K T S Q Q E H V Y E A A R O

1101 CCATTTTGA CCCCCTCCCT GGCCTCAATT TTGATTACTG GCAGGAATAG TGGAGGAAGG GGGGTGTGGC ACAGACCCAA TCCTAAGGCC GGAGGCCTTC
GGTA AAAACT GGGGCAGGA CGGAGTTAA AACTAATGAC CGTCTTTTAC ACCTCTTCC CCCCACACCG TGCTGCGGT AGGATTCGG CCTCCGGAAG

1201 AGGTCAGGA CATAGCTGCC TTCCCTCTCT CAGGCACCT CTGAGGTTCT TTTGGCCTC TGAACACANA GGATAATTGA GATCCATCTG CCTTCTGCTT
TCCAGTCTCT GTATCGACGG AAGGAGAGA GTCCGTGGAA GACTCCACA AACCAGGAG ACTTGTGTTT CCTATTAAAT CTAGGTAGAC GGAAGACGAA

1301 CCAGAAATCCC TGGGTGGTAG GATCCTGATA ATTAATTGCC AAGNATTGAG GCAGNAGGCT GGGAAACACG GACCACAGCC CCAAGTCCCT TCTTATGGGT
GGTCTTAGG ACCCACCATC CTAGGACTAT TAATTAACG TTCTTAACTC CGTCTTCCCA CCTTTGCTC CTGCTGTGCG GGTTCAGGGA AGAATACCCA

1401 GGTGGGCTCT TGGGCCATAG GGCACATGCC AGAGAGGCCA ACGACTCTGG AGAACCATG AGGTGGCCA TCTTCGCAAG TGGCTGCTCC AGTGATGAGC
CCACCCGAGA ACCCGGTATC CCGGTATCCG TCTCTCCGT TCCTGAGACC TCTTTGTGAC TCCCACCGGT AGAAGCGTTC ACCGACGAG TCACTACTCG

1501 CAACCTCCCA GAATCTGGGC AACAACTACT CTGATGAGCC CTGCATAGGA CAGGAGTACC AGATCATCGC CCAGATCAAT GGCAACTACG CCCGCTGCT
GTTGAAGGT CTAGACCCG TTGTTGATGA GACTACTCG GACGTATCT GTCTCATGG TCTAGTAGCG GGTCTAGTTA CCGTTGATGC GGGCGGACGA

FIG. 6B

SEQ ID NO:7

1601 GGACACAGTT CCTCTGGATT ATGAGTTTCT GCCCACTGAG GGCAAAAGTG TCTGTTAAAA ATGCCCCATT AGCCAGGAT CTGCTGACAT AATTGCTAG
CCTGTGTCIA GGAGACCTAA TACTCAAGA CCGGTACTC CCGTTTAC AGACAATTTT TACGGGTAA TCCGGTCTTA GACGACTGA TTAACGATC

1701 TCAGTCCCTG CCTTCTGCAT GGCTTCTTC CCTGCTACCT CTCTTCCTGG ATAGCCCCAA GTGTCCGCT ACCAACACTG GAGCCGCTGG GAGTCACTGG
AGTCAGGAAC GGAAGACGTA CCGGAAGAAG GGACGATGA GAGAAGGACC TATCGGGTTT CACAGGCCGA TGGTTCTGAC CTCGGCGACC CTCAGTGACC

1801 CTTTGCCCTG GAATTTGCCA GATGCATCTC AAGTAAGCCA GCTGCTGGAT TTGGCTCTGG GGCCTTCTAG TATCTCTGCC GGGGGCTTCT GGTACTCCTC
GAAACGGGAC CTTAAACGGT CTACGTAGAG TTCATTCCGT CGACGACCTA AACCGAGACC CGGAAGATC ATAGAGACGG CCCCCGAAGA CCATGAGGAG

1901 TCTAAATACC AGAGGGAGA TGCCCATAGC ACTAGGACTT GGTCACTATG CCTACAGACA CTATTCNACT TTGGCATCTT GCCACCAGAA GACCCGAGGG
AGATTTATGG TCTCCCTTCT ACGGTATCG TGATCCTGAA CCAGTAGTAC GGATGCTGT CATAGTTGA AACCGTAGAA CCGTGGTCTT CTGGGCTCCC

2001 AGGCTCAGT CTGCCAGCTC AGAGGACCAG CTATATCCAG GATCATTTCT CTTTCTTCAG GGCAGACAG CTTTAAATG AATGCTTAT TTCACAGGCC
TCCGAGTCCA GACGGTCGAG TCTCCTGTC GATATAGGTC CTAGTAAAGA GAAAGAGTC CCGTCTGTC GAAATTAAC TTTAACAATA AAGTGTCCGG

2101 AGGGTTCACT TCTGCTCCTC CACTATAAGT CTATGTTTCT GACTCTCTCC TGCTGCTCMA TAAATATCTA ATCATACAG C
TCCCAAGTCA AGACGAGGAG GTGATATTCA GATTACAAGA CTGAGAGAGG ACCACGAGTT ATTTATAGAT TAGTATTGTC G

FIG._6C

SEQ ID NO:8

CCCAGAAGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCTCGACCTCCT
CAGAGCAGCCGGCTGCCGCCCGGGAAGATGGCGAGCAGGAGCCGCCACCGCCTCCTCCT
GCTGCTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGC
CCCAAAGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAA
AACCCCAAAGAAGACTGTTTCCTCCAGATTAGAGTGGAAGAACTGGGTCGGAGTGTCTC
CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGA
TTTCAATATCCGGATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGT
TAGTGCCCCATCTGAGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATT
AGTGGCTCCAGCAGTTCCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAAGTGTGGT
AGAGCTACGATGTCAAGACAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGA
TGGCATCCGTTTGCTAGAAAATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACAC
AATGAATACAAAACCTGGAAGTCTGCAATTTAATACTGTTTCCAACTGGACACTGGAGA
ATATTCCTGTGAAGCCCGCAATTCTGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCA
AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGAT
TTCCGTTTGTGGCCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTTCAAAGAAAC
CTCCTTCCAGAAGAGTAATTCTTCATCTAAAGCCACGACAATGAGTGAAAATGTGCAGTG
GCTCACGCCTGTAATCCCAGCACTTTGGAAGGCCGCGCGGGCGGATCACGAGGTCAGGA
GTTCTAGACCAGTCTGGCCAATATGGTGAAACCCCATCTCTACTAAAATACAAAATTAG
CTGGGCATGGTGGCATGTGCCTGCAGTTCAGCTGCTTGGGAGACAGGAGAATCACTTGA
ACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGCCACTGCAGTCCAGCCTGGGTAA
CAGAGCAAGATTCCATCTCAAAAATAAAATAAATAAATAAATAAATACTGGTTTTTACC
TGTAGAATTCTTACAATAAATATAGCTTGATATTC

FIG._7

SEQ ID NO:9

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSR
LEWKKLGRSVSFVYYQOTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN
LEEDTVTLEVLVAPAVPSCVPPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR
LGSQSTNSSYTMNTKTGTTLQFNTVSKLDTGEYSCEARNSVGYYRRCPGKRMQVDDLNISGI
IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALW
KAAAGGSRGQEF

FIG._11

SEQ ID NO:5

1 GCAGGCAAG TACCAGGGCC GCCTGCATGT GAGCCACMAG GTTCCAGGAG ATGTATCCCT CCATTGAGC ACCTGGAGA TGGATGACCG GAGCCACTAC
CGTCCGTTTC ATGCTCCCGG CGGACGTACA CTCGGTGTTT CMAAGTCTC TACATAGGA GGTAACTCG TGGACCTCT ACCTACTGGC CTCGGTGATG
^42257.f1 SEQ ID NO:18 ^42257.p1 SEQ ID NO:22

101 ACGTGTGAAG TCACCTGGCA GACTCCTGAT GGCNACCAG TCGTGAGAGA TAAGATTACT GAGTCCGTG TCCAGAACT CTCTGTCTCC AAGCCCACAG
TGCACACTTC AGTGGACCGT CTGAGGACTA CCGTTGGTTC AGCACTCTCT ATTCTAATGA CTCGAGGCAC AGGTCTTTGA GAGACAGAGG TTCGGGTCTC

201 TGACAACTGG CAGCGGTTAT GGCTTCACGG TCCCCCAGG AATGAGGATT AGCCTTCAAT GCCAGGTTT CCGGTTCTCC TCCCATCAGT TATATTGGT
ACTGTTGACC GTCCCAATA CCGAAGTGCC ACGGGTGCC TTACTCCTAA TCGGAAGTTA CCGTCCCAAG CCCCAGAGG AGGCTAGTCA ATATAAACCA

301 ATAAGCAACA GACTAATAAC CAGGGAACCC ATCAAGTAG CAACCCTAAG TACCTTACTC TTCMAGCCTG CCGTGATAGC CGACTCAGG TCCTATTCT
TATTGTTGT CTGATTATTG GTCCCTTGGG TAGTTTCATC GTTGGGATTC ATGGAATGAG AAGTTCGGAC GCCACTATCG GCTGAGTCCG AGGATAAAGA

401 GCACTGCCAA GGGCAGGTT GGCTCTGACC AGCAGCGA CATTGTGAAG TTTGTGTCA AAGACTCCTC AAGCTACTC AAGACCAAGA CTGAGGCACC
CGTGACGGTT CCGGTCCAA CCGAGACTCG TCGTGTGGCT GTACACATTC GTACACATTC AAMACACAGT TTCTGAGGAG TTTCGATGAG TTCTGGTTCT GACTCCGTGG
^42257.f1 SEQ ID NO:20

501 TACAACCATG ACATACCCCT TGAAAGCAAC ATCTACAGTG AAGCAGTCCT GGGACTGGAC CACTGACATG GATGGCTACC TTGGAGAGAC CAGTGCTGG
ATGTTGGTAC TGTATGGGA ACTTTCGTTG TAGATGTCAC TTCGTACGGA CCCTGACCTG GTGACTGTAC CTACCGATGG AACCTCTCTG GTCACGACCC

601 CCAGGAAAGA GCCTGCCTGT CTTGCCATC ATCTCATCA TCTCCTTGTG CTGTATGGTG GTTTTACCA TGGCTATAT CATGCTCTGT CGGAAGACAT
GGTCTTTCT CGGACGGACA GAAACGGTAG TAGGAGTAGT AGAGGAACAC GACATACCAC CAAAAATGTT ACCGATATA GTACGAGACA GCCTTCTGTA
^42257.f2 SEQ ID NO:19

701 CCCAACAGA GCATCTCTAC GAAGCAGCCA GGGCACATGC CAGAGAGGCC AAGCACTCTG GAGAAACCAT GAGGTGGCC ATCTTCGCA GTGGCTGCTC
GGTGTGTTCT CGTACAGATG CTTGCTCGGT CCGGTGTACG GTCTCTCCGG TTGCTGAGAC CTCTTTGGTA CTCCACCCG TAGAAGCGTT CACCGACGAG

FIG._9A

SEQ ID NO:5

801 CAGTGATGAG CCAACTTCCC AGAATCTGGG GCACAACATA CTCTGATGAG CCTGTCATAG GACAGGAGTA CCAGATCATC GCCAGATCA ATGGCAACTA
GTCACTACTC GGTGAAGGG TCTTAGACCC CGTTGTTGAT GAGACTACTC GGGACGTATC CTGTCCTCAT GGTCTAGTAG CGGCTCTAGT TACCGTTGAT

901 CGCCCGCCTG CTGGACACAG TTCTCTCTGGA TTATGAGTTT CTGGCCACTG AGGCCAAGAAG TGCTGTGTTAA AAATGCCCA TTAGGCCAGG ATCTGCTGAC
GCGGGCGGAC GACCTGTGTC AAGGAGACCT AATACTCAAA GACCGGTGAC TCCCGTTTC ACAGACAAAT TTTACGGGGT AATCCGGTCC TAGACGACTG

1001 ATAATTGCCT AGTCAGTCTT TGCCTTCTGC ATGGCCTTCT TCCCTGCTAC CTCTCTTCCCT GGATAGCCCA AAGTGTCCGC CTACCAACAC TGGAGCCGCT
TATTAACGGA TCAGTCAGGA ACGGAAGACG TACCGGAAGA AGGACGATG GACAGAAGGA CCTATCGGT TTCACAGGCG GATGGTTGTG ACCTCGGCGA

1101 GGGAGTCACT GGCTTTGCCC TGGAAATTTGC CAGATGCATC TCAAGTAAGC CAGCTGCTGG ATTTGGCTCT GGGCCCTTCT AGTATCTCTG CCGGGGGCTT
CCCTCAGTGA CCGAAACGGG ACCTTAAACG GTCTACGTAG AGTTCATTCC GTCCAGGACC TAAACCGAGA CCGGGGAAGA TCATAGACAC GCGCCCGGAA
^42257.r2 SEQ ID NO:21

1201 CTGTACTCC TCTTAATA CCAGAGGGAA GATGCCCATTA GCACTAGGAC TTGTCATCA TGCTACAGA CACTATTCAA CTTTGGCATC TTGCCACCAG
GACCATGAGG AGAGATTTAT GGTCTCCCTT CTACGGCTAT CGTGATCTG AACCATGATG ACGATGTCT GTGATAAGTT GAAACCGTAG AACGGTGGTC

1301 AAGACCCGAG GGGAGGCTCA GCTCTGCCAG CTCAGAGGAC CAGCTATATC CAGGATCATT TCTCTTCTT CAGGGCCAGA CAGCTTTTAA TTGAAATTGT
TTCTGGGCTC CCTCCGAGT CGAGACGGTC GAGTCTCCTG GTCGATATAG GTCCTAGTAA AGAGAAAGAA CTCCCGGTCT GTCGAAATTT AACTTTAACA

1401 TATTTACAG GCCAGGGTTC AGTCTGCTC CTCCACTATA AGTCTAATGT TCTGACTCTC TCCTGGTGCT CAATAAATAT CTAATCATAA CAGCAAAAA
ATAAGTGT CCGTCCCAAG TCAAGACGAG GAGGTGATAT TCAGATTACA AGACTGAGAG AGGACCACGA GTTATTATA GATTAGTATT GTCGTTTTTT

1501 AAA
TTT

FIG._9B

A33_HUMAN A33 ANTIGEN PRECURSOR - HOMO SAPIENS FRAME SCORE MATCH PCT
+1 246 81 30

A33_HUMAN - A33 ANTIGEN PRECURSOR - HOMO SAPIENS (319 aa)

SCORE = 246 (86.6 BITS), EXPECT = 2.8e-19, P = 2.8e-19

IDENTITIES = 81/268 (30%), POSITIVES = 131/268 (48%), AT 121,17, FRAME = +1

DNA40628 121 LALGSVTVHSSEPEVRIPENNPVKLSAYSGFSSPR--VIEW-KFDQGDTRLVC--YNN
SEQ ID NO:23

A33_human 17 VTVD AISVETPQDVL RASQGSVTL PCTYHTSTSSREGLIQWDKLLLTHTERVVIWPFNS
SEQ ID NO:24

DNA40628 283 K--ITAS-YEDRVTFI-----PTGITFKSVTREDTGTYTCMV-----EEGNSYGEVKKV
* * * * * * * * * * * * * * * * *

A33_human 77 KNYIHGELYKNRVSISNNAEQSDASITIDQLTMADNGTYECSVSLMSDLEGNT--KSRVR

DNA40628 427 LIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPSEYTWFKDGIVMPTNPKSTRAFSN
* * * * * * * * *

A33_human 135 LLVLVPPSKPEGIEGETIIGNNIQLTCQSKESGPTPQYSWKRYNINLQEQP-----

DNA40628 607 SSYVLNPTTGELV-FDPLSADTGEYSCEARNGYGTPMTSNVRMEAVERNVGV---IVA
* * * * *

A33_human 187 ---LAQPASGQPVSLKNISTDTSGYICTSSNEEGTQFCNITVAVRSPSMNVALYVGI
* * * * *

DNA40628 775 AVLVTLLILLGILVFGIWFAYSRGHFDRT--KKGTSSKKVIYSQP

A33_human 244 GVVAALIIIGIIYY---CCCCRGKDDNTEDKEDARPNREAYEEP

FIG.-10A

SCORE = 245 (86.2 BITS), EXPECT = 3.6e-19, P = 3.6e-19
IDENTITIES = 83/273 (30%), POSITIVES = 131/273 (47%), AT 112,12, FRAME = +1

```
DNA40628 112 LC SL--ALGSVTVHSSEPEVRIPENNPVKLS CAYSGFSSPR---VEW-KFDQGD TTRLVC
SEQ ID NO:25
A33 human 12 LCAVRVTVD AISVETPQDVL RASQKSVTL PCTYHTSTSSREG LIQWDKLL LTHTERVVI
SEQ ID NO:26

DNA40628 274 --YNNK--ITAS-YEDRV TFL-----PTGITFKSV TREDTGTYTCMVSEEGGNSYGEVK
A33_human 72 WPF SNKNIYHGEL YKNRVSI SNNAEQDASITIDQLTMADNGTYECSVSLMS-DLEGNTK

DNA40628 421 --VKLIVLP PPKPTVNI PSSATIGNRAVLT CSEQDGSPPSEYTWFKDGI VMP TNP KSTR
A33_human 131 SRVRLVLV PPSKPECGIEGETIIGNNIQLTCQSKEGSPTPOYSWKRYN ILNQEQP----

DNA40628 595 AFSNSSYVLNPTTGELV-FDPLSASDTGEYSCEARNGYGTPMTSNAV RMEAVERNVGV--
A33_human 187 -----LAQPASGQPVSLKNISTDTSGYICTSSNEEGTQFCNITVAVRSPSMNVALYV

DNA40628 766 -IVA AVLVT LILLGILVFGIWFAYS RGHFDR T--KKG TSSKKVIYSQP
A33_human 240 GIAVGVAALIIIGIIY---CCCCRGKDDNTEDKEDARPNREAYEEP
```

FIG._10B

FIG. 12

SEQ ID NO: 6	A33_hum	1	M	V	G	K	M	W	P	V	L	W	T	L	C	A	V	R	V	T	V	D	A	I	S	V	E	T	P	Q	D	V	L	R	A	S	Q	G	K	S	V	T	L	P	C	T	Y	H	T	S	T	S
SEQ ID NO: 2	45416	1	.	M	G	I	L	L	G	L	L	L	G	H	L	T	V	D	T	Y	G	R	P	I	L	E	V	P	E	S	V	T	G	P	W	K	G	.	D	V	N	L	P	C	T	Y	D	P	L	O	G	
	A33_hum	51	S	R	E	G	L	I	O	W	D	K	L	L	T	H	T	E	R	V	V	I	W	.	P	F	S	N	K	N	Y	I	H	G	E	L	Y	K	N	R	V	S	I	S	N	N	A	E	Q	S	D	
	45416	49	Y	T	Q	V	L	V	K	W	.	.	L	V	O	R	G	S	D	P	V	T	I	F	L	R	D	S	S	G	D	H	I	Q	Q	A	K	Y	Q	G	R	L	H	V	S	H	K	V	.	P	G	D
	A33_hum	100	A	S	I	T	I	D	O	L	T	M	A	D	N	G	T	Y	E	C	S	V	S	.	L	M	S	D	L	E	G	N	T	K	S	R	V	R	L	L	V	L	V	P	P	S	
	45416	96	V	S	L	Q	L	S	T	L	E	W	D	O	R	S	H	Y	T	C	E	V	T	W	Q	T	P	D	G	N	O	V	V	R	D	K	I	T	E	L	R	V	Q	K	L	S	V	S	K	P	T	V
	A33_hum	143	K	P	E	C	G	I	E	G	E	T	I	G	N	I	Q	L	T	C	Q	S	K	E	G	S	P	T	P	Q	Y	S	W	K	R	Y	N	I	L	N	Q	E	Q	P	L	A	O	P	A	S		
	45416	146	T	T	G	S	G	Y	G	F	T	V	P	Q	M	R	I	S	L	Q	C	Q	A	R	.	G	S	P	I	S	I	W	.	.	Y	K	Q	T	N	N	Q	E	P	I	K	V	A	T				
	A33_hum	193	G	O	P	V	S	L	K	N	I	S	T	D	T	S	G	Y	I	C	T	S	S	N	E	E	G	T	.	Q	F	C	N	I	.	T	V	A	V	R	S	P	S	M	N	V	A	L	Y	V	G	
	45416	193	L	S	T	L	L	F	K	P	A	V	I	A	D	S	G	S	Y	F	C	T	A	K	G	Q	V	G	S	E	Q	H	S	D	I	V	K	F	V	V	K	D	S	S	K	L	L	K	T	K	T	E
	A33_hum	241	I	A	V	G	V	V	A	A	L	I	I	G	I	I	Y	C	C	C	C	R	G	K	D	D	N	T	E	D	K	E	D	A	R	P	N	R	E	A	Y	E	E	P	P	E	Q	L	R	E		
	45416	243	A	P	T	T	M	T	Y	P	L	K	A	T	S	T	V	K	Q	S	W	D	W	T	T	D	M	D	G	Y	L	G	E	T	S	A	G	P	G	K	S	L	P	V	F	A	I	I	I	S		
	A33_hum	291	L	S	R	E	R	E	E	E	O	D	Y	R	Q	E	E	O	R	S	T	G	R	E	S	P	D	H	L	D	Q																					
	45416	293	L	C	C	H	V	V	F	T	M	A	Y	I	M	L	C	R	K	T	S	O	Q	E	H	V	Y	E	A	A	R																					

FIG._13

SEQ ID NO: 6	A33_hum	1	..MVGKMWPV	L	WT	L	CAVR	V	T	V	D	...	A	I	S	V	E	T	P	Q	D	V	L	R	A	S	Q	G	K	S	V	T	L	P	C																
SEQ ID NO: 9	35638	1	MARRSRHRL	L	L	L	RYLV	V	A	L	G	Y	H	K	A	Y	G	F	S	A	P	K	D	Q	Q	V	V	T	A	V	E	Q	E	A	I	L	A	C													
	A33_hum	44	T	Y	H	T	S	S	R	E	G	L	I	Q	W	D	K	L	L	T	H	T	E	R	V	V	I	W	P	F	S	N	K	N	Y	I	H	G	E	L	Y	K	N	R	V	S	I	S	N		
	35638	51	..K	T	P	K	K	T	V	S	S	R	L	E	W	K	K	L	...	G	R	S	V	S	F	V	Y	Y	Q	O	T	..L	Q	G	D	..F	K	N	R			
	A33_hum	94	N	A	E	Q	S	D	A	S	I	T	I	D	Q	L	T	M	A	D	N	G	T	Y	E	C	S	V	S	L	M	S	D	L	E	G	N	..T	K	S	R	V	R	L	L	V	L	V	P	P	S
	35638	87	..A	E	M	I	D	F	N	I	R	I	K	N	V	T	R	S	D	A	G	K	Y	R	C	E	V	S	A	P	S	E	Q	G	N	L	E	E	D	T	V	T	L	E	V	L	V	A	P	A	
	A33_hum	143	K	P	E	C	G	I	E	G	E	T	I	G	N	I	Q	L	T	C	Q	S	K	E	G	S	P	T	P	Q	Y	S	W	K	R	Y	N	I	L	N	Q	E	Q	P	L	A	Q	P	A	S	
	35638	136	V	P	S	C	E	V	P	S	S	A	L	S	G	T	V	V	E	L	R	C	Q	D	K	E	G	N	P	A	P	E	Y	T	W	F	K	D	G	I	R	L	E	N	P	R	L	G	S	O	S
	A33_hum	193	G	Q	P	V	S	L	K	N	I	S	T	D	T	S	G	Y	I	C	T	S	S	N	E	E	G	T	Q	F	C	N	I	T	V	A	V	...	R	S	P	S	M	N	V	A	L	Y	V		
	35638	186	T	N	S	Y	T	M	N	T	K	T	G	T	L	Q	F	N	T	..V	S	K	L	D	T	G	E	Y	S	C	E	A	R	N	S	V	G	Y	R	R	C	P	G	K	R	M	Q	V	D		
	A33_hum	240	G	I	A	V	G	V	V	A	A	L	I	I	I	G	I	I	I	Y	C	C	...	C	R	G	K	D	D	N	T	E	D	K	E	D	A	R	P	N	R	E	A	Y	E	E	P	P	E		
	35638	235	L	N	I	S	G	I	I	A	A	V	V	V	A	L	V	I	S	V	C	G	L	G	V	C	Y	A	O	R	K	G	Y	F	S	K	E	T	S	F	O	K	S	N	S	S	K	A	T	T	
	A33_hum	287	Q	L	R	E	L	S	R	..E	R	E	E	E	D	D	Y	R	Q	E	E	Q	R	S	T	G	R	E	S	P	D	H	L	D	Q																
	35638	285	M	S	E	N	V	O	W	L	T	P	V	I	P	A	L	W	K	A	A	A	G	G	S	R	G	Q	E	F																					

FIG.-14

SEQ ID NO: 10 jam 1 MGT E G K A G R K L L F L F T - S M I L G S L V Q G K G S V Y T A Q S D V Q V P E N E S I K L T C
 SEQ ID NO: 1 40628 1 MGT K A Q V E R K L L C L F I L A I L L C S L A L G S V T V H S S E P E V R I P E N N P V K L S C

jam 50 T Y S G F S S P R V E W K F V Q G S T T A L V C Y N S Q I T A P Y A D R V T F S S S G I T F S S V T
 40628 51 A Y S G F S S P R V E W K F Q G D T T R L V C Y N N K I T A S Y E D R V T F L P T G I T F K S V T

jam 100 R K D N G E Y T C M V S E E G G Q N Y G E V S I H L T V L V P P S K P T I S V P S S V T I G N R A V
 40628 101 R E D T G T Y T C M V S E E G G N S Y G E V K V K L I V L V P P S K P T V N I P S S A T I G N R A V

jam 150 L T C S E H D G S P P S E Y S W F K D G I S M L T A D A K K T R A F M N S S F T I O P K S G D L I F
 40628 151 L T C S E Q D G S P P S E Y T W F K D G I - V M P T N P K S T R A F S N S S Y V L N P T T G E L V F

jam 200 D P V T A F D S G E Y Y C Q A Q N G Y G T A M R S E A A H M D A V E L N V G G I V A A V L V T L I L
 40628 200 D P L S A S D T G E Y S C E A R N G Y G T P M T S N A V R M E A V E R N V G V I V A A V L V T L I L

jam 250 L G L L I F G V W F A Y S R G Y F E T T K K G T A P G K K V I Y S Q P S T R S E G E F K Q T S S F L
 40628 250 L G I L V F G I W F A Y S R G H F D R T K K G T - S S K K V I Y S Q P S A R S E G E F K Q T S S F L

jam 300 V
 40628 299 V

FIG. 15

20 / 24

SEQ ID NO: 10 jam 1 M G T E G K A G R K L L F L F T S M I L G S L V O G K G S V Y T A Q S D V Q V P E N E S I K L T
 SEQ ID NO: 2 45416 1 M G I L L G L L L G H L T V D T Y G R P I L E V P E S V T G P W K G D V N L P

jam 49 C T Y S . . . G F S S P R V E W K F V Q G S T T A L V . . . C Y N S Q I T A P Y A D R V T F S .
 45416 41 C T Y D P L Q G Y T Q V L V K W L V Q R G S D P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H

jam 90 S S G I T F S S V T R K D N G E Y T C M V . . . S E E G G Q N Y G E V S I H L T V L V P P .
 45416 91 K V P G D V S L Q L S T L E M D D R S H Y T C E V T W Q T P D G N Q V V R D K I T E L R V Q K L S V

jam 132 S K P T I S V P S . . . S V T I G N R A V L T C S E H D G S P P S E Y S W F K O G I S M L T A D A
 45416 141 S K P T V T T G S G Y G F T V P Q G M R I S L O C Q A R . G S P P I S Y I W Y K Q Q T N . . N Q E P

jam 178 K K T R A F M N S S F T I D P K S G D L I F D P V T A F D S G E Y Y C Q A Q N G Y G T A M R S E A A
 45416 188 I K V A T L S T L L F K P A V I A D S G S Y F C T A K G O V G S E Q H S D I V

jam 228 H . . . M D A V E L N V G G I V A A V L V T L I L L G L L I F G . . . V W F A Y S R G Y F E T T K K
 45416 227 K F V V K D S S K L L K T K T E A P T T M T Y P L K A T S T V K O S W D W T T D M D G Y L G E T S A

jam 272 G T A P G K K V I Y S O P S T R S E G E F K Q T S S F L V
 45416 277 G P G K S L P V F A I I L I I S L C C M V V F T M A Y I M L C R K T S Q O E H V Y E A A R

FIG. 16

+

SEQ ID NO: 10 jam 1 M G T E G K A G R K L L F L F T S M I L G S L V O G K G S V Y T A Q S D V Q V . . . P E N E S I K L
 SEQ ID NO: 29 35638 1 . . . M A R R S R H R L L L L R Y L V V A L G Y H K A Y G F S A P K Q Q V T A V E Y O E A I L

jam 48 T C . T Y S G F S S P R V E W K F V O G S T T A L V C Y N S Q I T A P Y A D R V T F S S S G I T F S
 35638 49 A C K T P K K T V S S R L E W K K L . G R S V S F V Y Y Q Q T L Q G D F K N R A E M I D F N I R I K

jam 97 S V T R K D N G E Y T C M V S . . E E G G Q N Y G E V S I H L T V L V P P S K P T I S V P S S V T I
 35638 98 N V T R S D A G K Y R C E V S A P S E Q G Q N L E E D T V T L E V L V A P A V P S C E V P S S A L S

jam 145 G N R A V L T C S E H D G S P P S E Y S W F K D G I S M L T A D A K K T R A F M N S S F T I D P K S
 35638 148 G T V V E L R C O D K E G N P A P E Y T W F K D G I R L L . E N P R L G S Q S T N S S Y T M N T K T

jam 195 G D L I F D P V T A F D S G E Y Y C Q A Q N G Y G T A M R S E A A H M D A V E L N V G I V A A V L
 35638 197 G T L Q F N T V S K L D T G E Y S C E A R N S V G . Y R R C P G K R M Q V D D L N I S G I I A A V V

jam 245 V T L I L L G L L I F G V W F A Y S R G Y F E T T K K G T A P G K K V I Y S Q P S T R S E G E F K Q
 35638 246 V V A L V I S V C G L G V C Y A Q R K G Y F . . . S K E T S F O K S N S S S K A T T M S E N V Q W L

jam 295 T S S F L V
 35638 293 T P V I P A L W K A A A G G S R G Q E F

FIG._17

+

SEQ ID NO: 6	A33_hum	1MVGKMWPVLWT.LCAVRVTVDALSVETPQDVLRASQGKSVTL	PCT
SEQ ID NO: 10	jam	1	MGTEGKAGRKLLFLFTSMILGSLVOGKGSVYTAQSDVQVPENESIKLTCT	
A33_hum		45	YHTSTSSREGLIQWDKLLLTHTERVVIWPFSSKNYIHGELYKNRVSISNN	
jam		51	YSGFSSPR...VEW.KFVOGSTTALVC..YNSQ...ITAP.YADRVTFSS.	
A33_hum		95	AEQSDASITIDQLTMAONGTYECSVSLMSDLEGNTKSRVRL	LVLVPPSPKP
jam		91SGITTFSSVTRKDNGETYTCMVSEEGG.QNYGEVSIHL	TVLVPPSPKP
A33_hum		145	ECGIEGETIIGNNIO LTCQSKESGPTPOYSWKRYNINLQEQPLAQPASGQ	
jam		135	TISVPSSVTIGNRAVLTCSEHDGSPSEYSWFKOGISMLTADAKKTRAFM	
A33_hum		195	PVSLKNISTDTSGYYICTSSNEEGTQFCN.....ITVAVRSPSMN...VAL	
jam		185	NSSFTIDPKSGDLIFDPVTAFDSGEYYCQAQNGYGTAMRSEAAHMDAVEL	
A33_hum		238	YV.GIAGVGVAAALIIIGIIICYC...CCCRGKDDNTEDKEDARPNREAYEE	
jam		235	NVGGIVAAVLVTLLGLLIFGVWFAYSRGYFE.TTKKGTAPGKXVIYSQ	
A33_hum		284	PEQLRELSREREEEDDYRQEEQRSTGRESPOHLDQ	
jam		284	PTRSEGEFKQTSSFLV	

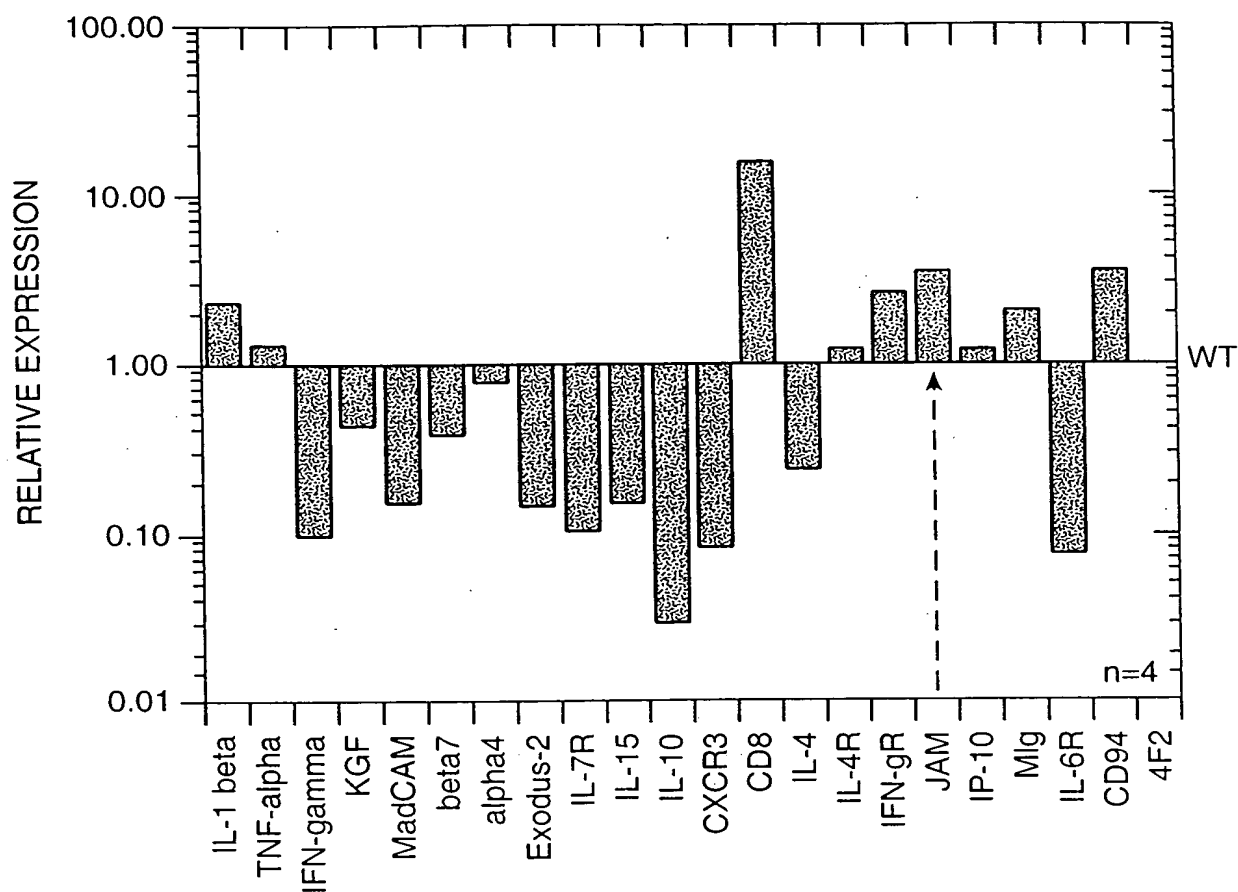
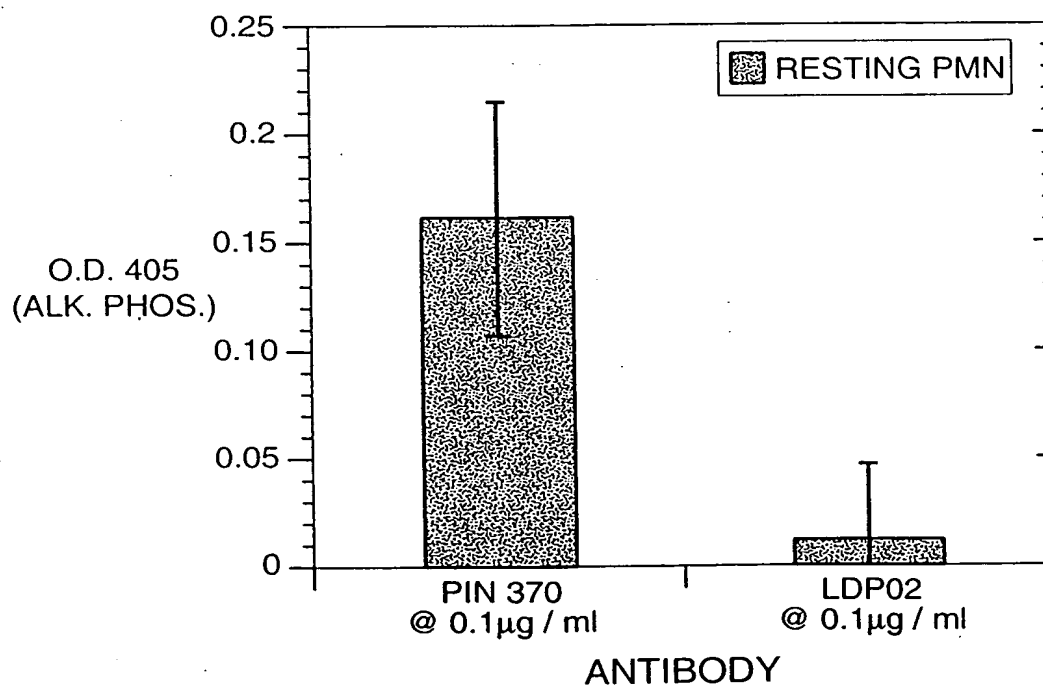
FIG.-18

23 / 24

<u>TISSUE</u>	<u>EXPRESSION</u>	<u>TISSUE</u>	<u>EXPRESSION</u>	<u>TISSUE</u>	<u>EXPRESSION</u>
WHOLE BRAIN	+	HEART	++	KIDNEY	+++
AMYGDALA	+	AORTA	+	LIVER	++
CAUDATE NUCLEUS	+	SKELETAL MUSCLE	+	SMALL INTESTINE	++
CEREBELLUM	-	COLON	+++	SPLEEN	++
CEREBRAL CORTEX	+	BLADDER	++	THYMUS	++
FRONTAL LOBE	+	UTERUS	+	PERIPHERAL LEUKOCYTE	+
HIPPOCAMPUS	+	PROSTATE	+++	LYMPH NODE	+
MEDULLA OBLONGATA	+	STOMACH	+++	BONE MARROW	+
OCCIPITAL LOBE	+	TESTIS	++		
PUTAMEN	+	OVARY	+++	APPENDIX	+
SUSTANTIA NIGRA	+	PANCREAS	++	LUNG	++++
TEMPORAL LOBE	+	PITUITARY GLAND	++	TRACHEA	++++
THALAMUS	+	ADRENAL GLAND	++	PLACENTA	++++
NUCLEUS ACCUMBEUS	+	THYROID GLAND	++		
SPINAL CORD	-	SALIVARY GLAND	+++	FETAL BRAIN	+
		MAMMARY GLAND	++	FETAL HEART	+
				FETAL KIDNEY	++
				FETAL LIVER	+++
				FETAL SPLEEN	+
				FETAL LUNG	++++

FIG._19

24 / 24

**FIG. 20****FIG. 21**